

#4

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/517,905  
Source: PCT/10  
Date Processed by STIC: 12/22/04

# ***ENTERED***

**CRF Errors Edited by the STIC Systems  
Branch**

Serial Number: 10/517,905

CRF Edit Date: 12/27/04  
Edited by: AZ

\_\_\_ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

\_\_\_ Corrected the SEQ ID NO. Sequence numbers edited were:

\_\_\_\_\_

\_\_\_ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

\_\_\_\_\_

\_\_\_ Deleted: \_\_\_ invalid beginning/end-of-file text ; \_\_\_ page numbers

\_\_\_ Inserted mandatory headings/numeric identifiers, specifically:

\_\_\_\_\_

\_\_\_ Moved responses to same line as heading/numeric identifier, specifically:

\_\_\_\_\_

\_\_\_ Other: Sequence 19 - corrected amino acid numbering

\_\_\_\_\_

\_\_\_\_\_



PCT10

## RAW SEQUENCE LISTING

DATE: 12/27/2004

PATENT APPLICATION: US/10/517,905

TIME: 13:40:27

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\12272004\J517905.raw

3 <110> APPLICANT: Oregon Health & Science University  
 4 Michael, Heinrich Charles  
 5 Corless, Christopher Lee  
 6 Fletcher, Jonathan Alfred  
 7 Demetri, George D.  
 9 <120> TITLE OF INVENTION: ACTIVATING MUTATIONS OF PLATELET DERIVED GROWTH FACTOR  
 RECEPTOR  
 10 ALPHA (PDGFRA) AS DIAGNOSTIC MARKERS AND THERAPEUTIC TARGETS  
 12 <130> FILE REFERENCE: 899-65892-02  
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/517,905  
 C--> 14 <141> CURRENT FILING DATE: 2004-12-10  
 14 <150> PRIOR APPLICATION NUMBER: US 60/389,107  
 15 <151> PRIOR FILING DATE: 2002-06-13  
 17 <150> PRIOR APPLICATION NUMBER: US 60/438,899  
 18 <151> PRIOR FILING DATE: 2003-01-08  
 20 <160> NUMBER OF SEQ ID NOS: 27  
 22 <170> SOFTWARE: PatentIn version 3.2  
 24 <210> SEQ ID NO: 1  
 25 <211> LENGTH: 6633  
 26 <212> TYPE: DNA  
 27 <213> ORGANISM: Homo sapiens  
 30 <220> FEATURE:  
 31 <221> NAME/KEY: CDS  
 32 <222> LOCATION: (395)..(3664)  
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 39 gagagaaact tttattttga agagaccaag gttgaggggg ggcttatttc ctgacagcta 180  
 41 tttacttaga gcaaatgatt agtttttagaa ggatggacta taacattgaa tcaattacaa 240  
 43 aacgcggttt ttgagcccat tactgttgga gctacagggg gagaaacagg aggagactgc 300  
 45 aagagatcat ttgggaaggc cgtgggcacg ctctttactc catgtgtggg acattcattg 360  
 47 cggaataaca tcggaggaga agtttcccg agct atg ggg act tcc cat ccg gcg 415  
 48 Met Gly Thr Ser His Pro Ala  
 49 1 5  
 51 ttc ctg gtc tta ggc tgt ctt ctc aca ggg ctg agc cta atc ctc tgc 463  
 52 Phe Leu Val Leu Gly Cys Leu Leu Thr Gly Leu Ser Leu Ile Leu Cys  
 53 10 15 20  
 55 cag ctt tca tta ccc tct atc ctt cca aat gaa aat gaa aag gtt gtg 511  
 56 Gln Leu Ser Leu Pro Ser Ile Leu Pro Asn Glu Asn Glu Lys Val Val  
 57 25 30 35  
 59 cag ctg aat tca tcc ttt tct ctg aga tgc ttt ggg gag agt gaa gtg 559  
 60 Gln Leu Asn Ser Ser Phe Ser Leu Arg Cys Phe Gly Glu Ser Glu Val  
 61 40 45 50 55  
 63 agc tgg cag tac ccc atg tct gaa gaa gag agc tcc gat gtg gaa atc 607

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67	aga	aat	gaa	gaa	aac	aac	agc	ggc	ctt	ttt	gtg	acg	gtc	ttg	gaa	gtg	655
68	Arg	Asn	Glu	Glu	Asn	Asn	Ser	Gly	Leu	Phe	Val	Thr	Val	Leu	Glu	Val	
69				75					80					85			
71	agc	agt	gcc	tcg	gcg	gcc	cac	aca	ggg	ttg	tac	act	tgc	tat	tac	aac	703
72	Ser	Ser	Ala	Ser	Ala	Ala	His	Thr	Gly	Leu	Tyr	Thr	Cys	Tyr	Tyr	Asn	
73			90					95					100				
75	cac	act	cag	aca	gaa	gag	aat	gag	ctt	gaa	ggc	agg	cac	att	tac	atc	751
76	His	Thr	Gln	Thr	Glu	Glu	Asn	Glu	Leu	Glu	Gly	Arg	His	Ile	Tyr	Ile	
77		105					110				115						
79	tat	gtg	cca	gac	cca	gat	gta	gcc	ttt	gta	cct	cta	gga	atg	acg	gat	799
80	Tyr	Val	Pro	Asp	Pro	Asp	Val	Ala	Phe	Val	Pro	Leu	Gly	Met	Thr	Asp	
81	120					125					130				135		
83	tat	tta	gtc	atc	gtg	gag	gat	gat	gat	tct	gcc	att	ata	cct	tgt	cgc	847
84	Tyr	Leu	Val	Ile	Val	Glu	Asp	Asp	Asp	Ser	Ala	Ile	Ile	Pro	Cys	Arg	
85					140					145					150		
87	aca	act	gat	ccc	gag	act	cct	gta	acc	tta	cac	aac	agt	gag	ggg	gtg	895
88	Thr	Thr	Asp	Pro	Glu	Thr	Pro	Val	Thr	Leu	His	Asn	Ser	Glu	Gly	Val	
89				155					160					165			
91	gta	cct	gcc	tcc	tac	gac	agc	aga	cag	ggc	ttt	aat	ggg	acc	ttc	act	943
92	Val	Pro	Ala	Ser	Tyr	Asp	Ser	Arg	Gln	Gly	Phe	Asn	Gly	Thr	Phe	Thr	
93			170					175					180				
95	gta	ggg	ccc	tat	atc	tgt	gag	gcc	acc	gtc	aaa	gga	aag	aag	ttc	cag	991
96	Val	Gly	Pro	Tyr	Ile	Cys	Glu	Ala	Thr	Val	Lys	Gly	Lys	Lys	Phe	Gln	
97		185					190					195					
99	acc	atc	cca	ttt	aat	gtt	tat	gct	tta	aaa	gca	aca	tca	gag	ctg	gat	1039
100	Thr	Ile	Pro	Phe	Asn	Val	Tyr	Ala	Leu	Lys	Ala	Thr	Ser	Glu	Leu	Asp	
101	200					205					210				215		
103	cta	gaa	atg	gaa	gct	ctt	aaa	acc	gtg	tat	aag	tca	ggg	gaa	acg	att	1087
104	Leu	Glu	Met	Glu	Ala	Leu	Lys	Thr	Val	Tyr	Lys	Ser	Gly	Glu	Thr	Ile	
105					220						225				230		
107	gtg	gtc	acc	tgt	gct	gtt	ttt	aac	aat	gag	gtg	gtt	gac	ctt	caa	tgg	1135
108	Val	Val	Thr	Cys	Ala	Val	Phe	Asn	Asn	Glu	Val	Val	Asp	Leu	Gln	Trp	
109				235					240					245			
111	act	tac	cct	gga	gaa	gtg	aaa	ggc	aaa	ggc	atc	aca	atg	ctg	gaa	gaa	1183
112	Thr	Tyr	Pro	Gly	Glu	Val	Lys	Gly	Lys	Gly	Ile	Thr	Met	Leu	Glu	Glu	
113			250					255					260				
115	atc	aaa	gtc	cca	tcc	atc	aaa	ttg	gtg	tac	act	ttg	acg	gtc	ccc	gag	1231
116	Ile	Lys	Val	Pro	Ser	Ile	Lys	Leu	Val	Tyr	Thr	Leu	Thr	Val	Pro	Glu	
117		265					270					275					
119	gcc	acg	gtg	aaa	gac	agt	gga	gat	tac	gaa	tgt	gct	gcc	cgc	cag	gct	1279
120	Ala	Thr	Val	Lys	Asp	Ser	Gly	Asp	Tyr	Glu	Cys	Ala	Ala	Arg	Gln	Ala	
121	280					285					290				295		
123	acc	agg	gag	gtc	aaa	gaa	atg	aag	aaa	gtc	act	att	tct	gtc	cat	gag	1327
124	Thr	Arg	Glu	Val	Lys	Glu	Met	Lys	Lys	Val	Thr	Ile	Ser	Val	His	Glu	
125					300						305				310		
127	aaa	ggt	ttc	att	gaa	atc	aaa	ccc	acc	ttc	agc	cag	ttg	gaa	gct	gtc	1375
128	Lys	Gly	Phe	Ile	Glu	Ile	Lys	Pro	Thr	Phe	Ser	Gln	Leu	Glu	Ala	Val	



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196	Ser	Arg	Trp	Glu	Phe	Pro	Arg	Asp	Gly	Leu	Val	Leu	Gly	Arg	Val	Leu	
197		585						590					595				
199	ggg	tct	gga	gcg	ttt	ggg	aag	gtg	gtt	gaa	gga	aca	gcc	tat	gga	tta	2239
200	Gly	Ser	Gly	Ala	Phe	Gly	Lys	Val	Val	Glu	Gly	Thr	Ala	Tyr	Gly	Leu	
201	600					605				610						615	
203	agc	cgg	tcc	caa	cct	gtc	atg	aaa	gtt	gca	gtg	aag	atg	cta	aaa	ccc	2287
204	Ser	Arg	Ser	Gln	Pro	Val	Met	Lys	Val	Ala	Val	Lys	Met	Leu	Lys	Pro	
205					620					625						630	
207	acg	gcc	aga	tcc	agt	gaa	aaa	caa	gct	ctc	atg	tct	gaa	ctg	aag	ata	2335
208	Thr	Ala	Arg	Ser	Ser	Glu	Lys	Gln	Ala	Leu	Met	Ser	Glu	Leu	Lys	Ile	
209				635					640							645	
211	atg	act	cac	ctg	ggg	cca	cat	ttg	aac	att	gta	aac	ttg	ctg	gga	gcc	2383
212	Met	Thr	His	Leu	Gly	Pro	His	Leu	Asn	Ile	Val	Asn	Leu	Leu	Gly	Ala	
213			650					655					660				
215	tgc	acc	aag	tca	ggc	ccc	att	tac	atc	atc	aca	gag	tat	tgc	ttc	tat	2431
216	Cys	Thr	Lys	Ser	Gly	Pro	Ile	Tyr	Ile	Ile	Thr	Glu	Tyr	Cys	Phe	Tyr	
217		665					670					675					
219	gga	gat	ttg	gtc	aac	tat	ttg	cat	aag	aat	agg	gat	agc	ttc	ctg	agc	2479
220	Gly	Asp	Leu	Val	Asn	Tyr	Leu	His	Lys	Asn	Arg	Asp	Ser	Phe	Leu	Ser	
221	680				685					690						695	
223	cac	cac	cca	gag	aag	cca	aag	aaa	gag	ctg	gat	atc	ttt	gga	ttg	aac	2527
224	His	His	Pro	Glu	Lys	Pro	Lys	Lys	Glu	Leu	Asp	Ile	Phe	Gly	Leu	Asn	
225			700						705							710	
227	cct	gct	gat	gaa	agc	aca	cgg	agc	tat	gtt	att	tta	tct	ttt	gaa	aac	2575
228	Pro	Ala	Asp	Glu	Ser	Thr	Arg	Ser	Tyr	Val	Ile	Leu	Ser	Phe	Glu	Asn	
229			715						720					725			
231	aat	ggt	gac	tac	atg	gac	atg	aag	cag	gct	gat	act	aca	cag	tat	gtc	2623
232	Asn	Gly	Asp	Tyr	Met	Asp	Met	Lys	Gln	Ala	Asp	Thr	Thr	Gln	Tyr	Val	
233			730					735					740				
235	ccc	atg	cta	gaa	agg	aaa	gag	gtt	tct	aaa	tat	tcc	gac	atc	cag	aga	2671
236	Pro	Met	Leu	Glu	Arg	Lys	Glu	Val	Ser	Lys	Tyr	Ser	Asp	Ile	Gln	Arg	
237		745					750					755					
239	tca	ctc	tat	gat	cgt	cca	gcc	tca	tat	aag	aag	aaa	tct	atg	tta	gac	2719
240	Ser	Leu	Tyr	Asp	Arg	Pro	Ala	Ser	Tyr	Lys	Lys	Lys	Ser	Met	Leu	Asp	
241	760				765					770						775	
243	tca	gaa	gtc	aaa	aac	ctc	ctt	tca	gat	gat	aac	tca	gaa	ggc	ctt	act	2767
244	Ser	Glu	Val	Lys	Asn	Leu	Leu	Ser	Asp	Asp	Asn	Ser	Glu	Gly	Leu	Thr	
245			780						785							790	
247	tta	ttg	gat	ttg	ttg	agc	ttc	acc	tat	caa	gtt	gcc	cga	gga	atg	gag	2815
248	Leu	Leu	Asp	Leu	Leu	Ser	Phe	Thr	Tyr	Gln	Val	Ala	Arg	Gly	Met	Glu	
249			795						800					805			
251	ttt	ttg	gct	tca	aaa	aat	tgt	gtc	cac	cgt	gat	ctg	gct	gct	cgc	aac	2863
252	Phe	Leu	Ala	Ser	Lys	Asn	Cys	Val	His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	
253			810					815					820				
255	gtc	ctc	ctg	gca	caa	gga	aaa	att	gtg	aag	atc	tgt	gac	ttt	ggc	ctg	2911
256	Val	Leu	Leu	Ala	Gln	Gly	Lys	Ile	Val	Lys	Ile	Cys	Asp	Phe	Gly	Leu	
257		825					830					835					
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264	Phe	Leu	Pro	Val	Lys	Trp	Met	Ala	Pro	Glu	Ser	Ile	Phe	Asp	Asn	Leu	
265					860					865					870		
267	tac	acc	aca	ctg	agt	gat	gtc	tgg	tct	tat	ggc	att	ctg	ctc	tgg	gag	3055
268	Tyr	Thr	Thr	Leu	Ser	Asp	Val	Trp	Ser	Tyr	Gly	Ile	Leu	Leu	Trp	Glu	
269					875				880						885		
271	atc	ttt	tcc	ctt	ggg	ggc	acc	cct	tac	ccc	ggc	atg	atg	gtg	gat	tct	3103
272	Ile	Phe	Ser	Leu	Gly	Gly	Thr	Pro	Tyr	Pro	Gly	Met	Met	Val	Asp	Ser	
273					890				895					900			
275	act	ttc	tac	aat	aag	atc	aag	agt	ggg	tac	cgg	atg	gcc	aag	cct	gac	3151
276	Thr	Phe	Tyr	Asn	Lys	Ile	Lys	Ser	Gly	Tyr	Arg	Met	Ala	Lys	Pro	Asp	
277		905					910				915						
279	cac	gct	acc	agt	gaa	gtc	tac	gag	atc	atg	gtg	aaa	tgc	tgg	aac	agt	3199
280	His	Ala	Thr	Ser	Glu	Val	Tyr	Glu	Ile	Met	Val	Lys	Cys	Trp	Asn	Ser	
281	920					925					930				935		
283	gag	ccg	gag	aag	aga	ccc	tcc	ttt	tac	cac	ctg	agt	gag	att	gtg	gag	3247
284	Glu	Pro	Glu	Lys	Arg	Pro	Ser	Phe	Tyr	His	Leu	Ser	Glu	Ile	Val	Glu	
285					940					945					950		
287	aat	ctg	ctg	cct	gga	caa	tat	aaa	aag	agt	tat	gaa	aaa	att	cac	ctg	3295
288	Asn	Leu	Leu	Pro	Gly	Gln	Tyr	Lys	Lys	Ser	Tyr	Glu	Lys	Ile	His	Leu	
289					955				960					965			
291	gac	ttc	ctg	aag	agt	gac	cat	cct	gct	gtg	gca	cgc	atg	cgt	gtg	gac	3343
292	Asp	Phe	Leu	Lys	Ser	Asp	His	Pro	Ala	Val	Ala	Arg	Met	Arg	Val	Asp	
293			970					975					980				
295	tca	gac	aat	gca	tac	att	ggg	gtc	acc	tac	aaa	aac	gag	gaa	gac	aag	3391
296	Ser	Asp	Asn	Ala	Tyr	Ile	Gly	Val	Thr	Tyr	Lys	Asn	Glu	Glu	Asp	Lys	
297		985					990				995						
299	ctg	aag	gac	tgg	gag	ggg	ggg	ctg	gat	gag	cag	aga	ctg	agc	gct		3436
300	Leu	Lys	Asp	Trp	Glu	Gly	Gly	Leu	Asp	Glu	Gln	Arg	Leu	Ser	Ala		
301	1000					1005					1010						
303	gac	agt	ggc	tac	atc	att	cct	ctg	cct	gac	att	gac	cct	gtc	cct		3481
304	Asp	Ser	Gly	Tyr	Ile	Ile	Pro	Leu	Pro	Asp	Ile	Asp	Pro	Val	Pro		
305	1015					1020					1025						
307	gag	gag	gag	gac	ctg	ggc	aag	agg	aac	aga	cac	agc	tcg	cag	acc		3526
308	Glu	Glu	Glu	Asp	Leu	Gly	Lys	Arg	Asn	Arg	His	Ser	Ser	Gln	Thr		
309	1030					1035					1040						
311	tct	gaa	gag	agt	gcc	att	gag	acg	ggg	tcc	agc	agt	tcc	acc	ttc		3571
312	Ser	Glu	Glu	Ser	Ala	Ile	Glu	Thr	Gly	Ser	Ser	Ser	Ser	Thr	Phe		
313	1045					1050					1055						
315	atc	aag	aga	gag	gac	gag	acc	att	gaa	gac	atc	gac	atg	atg	gac		3616
316	Ile	Lys	Arg	Glu	Asp	Glu	Thr	Ile	Glu	Asp	Ile	Asp	Met	Met	Asp		
317	1060					1065					1070						
319	gac	atc	ggc	ata	gac	tct	tca	gac	ctg	gtg	gaa	gac	agc	ttc	ctg		3661
320	Asp	Ile	Gly	Ile	Asp	Ser	Ser	Asp	Leu	Val	Glu	Asp	Ser	Phe	Leu		
321	1075					1080					1085						
323	taa	ctggcggatt	cgaggggttc	cttccacttc	tggggccacc	tctggatccc											3714
325	gttcagaaaa	ccactttatt	gcaatgcgga	ggttgagagg	aggacttggt	tgatgtttaa											3774

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Seq#:19; N Pos. 36432,36433,36774,36775,36776,36777,36778,36779,36780,36781  
Seq#:19; N Pos. 36782,36783,36784,36785,36786,36787,36788,36789,36790,36791  
Seq#:19; N Pos. 36792,36793,36794,36795,36796,36797,36798,36799,36800,36801  
Seq#:19; N Pos. 36802,36803,36804,36805,36806,36807,36808,36809,36810,36811  
Seq#:19; N Pos. 36812,36813,36814,36815,36816,36817,36818,36819,36820,36821  
Seq#:19; N Pos. 36822,36823,36824,36825,36826,36827,36828,36829,36830,36831  
Seq#:19; N Pos. 36832,36833,36834,36835,36836,36837,36838,36839,36840,36841  
Seq#:19; N Pos. 36842,36843,36844,36845,36846,36847,36848,36849,36850,36851  
Seq#:19; N Pos. 36852,36853,36854,36855,36856,36857,36858,36859,36860,36861  
Seq#:19; N Pos. 36862,36863,36864,36865,36866,36867,36868,36869,36870,36871  
Seq#:19; N Pos. 36872,36873  
Seq#:19; N Pos. 59740,59742,59743,59744,59749,59750,59751,59752,59753,59754  
Seq#:19; N Pos. 59755,59759,59760,59765,59766,59776,59777,59778,59779,59780



**RAW SEQUENCE LISTING ERROR SUMMARY**  
PATENT APPLICATION: US/10/517,905

DATE: 12/27/2004  
TIME: 13:40:28

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\12272004\J517905.raw

Seq#:19; N Pos. 59781,59782,59783,59784,59785,59786,59787,59788,59789,59790  
Seq#:19; N Pos. 59791,59792,59793,59794,59795,59796,59797,59798,59799,59800  
Seq#:19; N Pos. 59801,59802,59803,59804,59805,59806,59807,59808,59809,59810  
Seq#:19; N Pos. 59811,59812,59813,59814,59815,59816,59817,59818,59819,59820  
Seq#:19; N Pos. 59821,59822,59823,59824,59825,59826,59827,59828,59829,59830  
Seq#:19; N Pos. 59831,59832,59833,59834,59835,59836,59837,59838,59839,59840  
Seq#:19; N Pos. 59841,59842,59843,59844,59845,59846,59847,59848,59849,59850

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/10/517,905

DATE: 12/27/2004

TIME: 13:40:28

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\12272004\J517905.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No  
 L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
 L:4793 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 19  
 L:4901 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 19  
 L:4972 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:10557  
 M:341 Repeated in SeqNo=19  
 L:10171 M:361 W: Invalid Split Codon, Sequence data for SEQ ID#: 19  
 L:13371 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26 after pos.:2047  
 M:341 Repeated in SeqNo=26  
 L:13881 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27 after pos.:544  
 M:341 Repeated in SeqNo=27